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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/048,116	02/27/2002	Nicolas Glaichenhaus	1721-47	6350
23117	7590	03/24/2006	EXAMINER	
NIXON & VANDERHYE, PC 901 NORTH GLEBE ROAD, 11TH FLOOR ARLINGTON, VA 22203			DIBRINO, MARIANNE NMN	
			ART UNIT	PAPER NUMBER

1644

DATE MAILED: 03/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

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10/048,116

APPLICATION NO/ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER
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1644

01232006

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

Please find below a communication from the EXAMINER in charge of this application

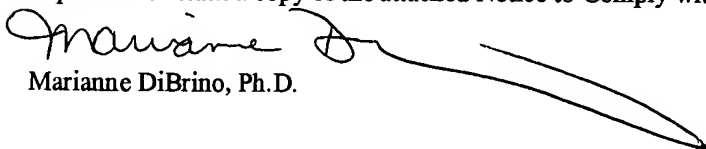
This application fails to comply with 37 C.F.R. 1.821-1.825 for the reason(s) listed on the Notice to comply with the sequence rules. The applicants are required to submit a new CRF and statement that the content of the paper and computer readable copies are the same, and where applicable, include no new matter.

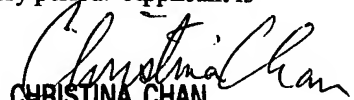
37 C.F.R. 1.821 (e) A copy of the "Sequence Listing" referred to in paragraph © of this section must also be submitted in computer readable form in accordance with the requirements of § 1.824. The computer readable form is a copy of the "Sequence Listing" and will not necessarily be retained as part of the patent application file. If the computer readable form of a new application is to be identical with the computer readable form of another application of the applicant on file in the Office, reference may be made to the other application and computer readable form in lieu of filing a duplicate computer readable form in the new application. The new application shall be accompanied by a letter making such reference to the other application and computer readable form, both of which shall be completely identified.

(f) In addition to the paper copy required by paragraph © of this section and the computer readable form required by paragraph (e) of this section, a statement that the content of the paper and computer readable copies are the same must be submitted with the computer readable form. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

Any inquiry concerning this communication should be directed to Examiner Marianne DiBrino, Art Unit 1644, whose telephone number is 571-272-0842.

APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.


Marianne DiBrino, Ph.D.


CHRISTINA CHAN
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Application No.: 10/048,116

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth at 37 C.F.R. 1.821 - 1.825 for the following reason(s):

 X 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

 X 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

 7. Other:

Applicant Must Provide:

 X A substitute computer readable form (CRF) copy of the "Sequence Listing".

 X A substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

 X A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-421

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/048,116A
Source: 1FJ/16
Date Processed by STIC: 12/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
Alexandria, VA 22314**

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/048,116A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☒ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) 2,4,6,8. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

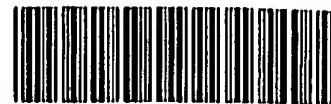
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:15

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6 FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7 IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
 11 <140> CURRENT APPLICATION NUMBER: 10/048,116A
 12 <141> CURRENT FILING DATE: 2002-02-27
 14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
 15 <151> PRIOR FILING DATE: 2000-07-28
 17 <150> PRIOR APPLICATION NUMBER: FR99/09862 *suggestion*
 18 <151> PRIOR FILING DATE: 1999-07-29
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn Ver. 2.0 *Please upgrade to PatentIn 3.3 (available at www.uspto.gov)*
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1517
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
 31 coding IAalpha(d)/Fc
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (18)..(1502)
 37 <400> SEQUENCE: 1
 38 aaagggggga attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc 50
 39 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
 40 1 5 10
 42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att 98
 43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
 44 15 20 25
 46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct 146
 47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
 48 30 35 40
 50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc 194
 51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
 52 45 50 55
 54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt 242
 55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
 56 60 65 70 75
 58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct 290
 59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
 60 80 85 90
 62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc 338

see p. 3 for error
Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:15

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

```

63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95          100          105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct 386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110          115          120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc 434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72          125          130          135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc 482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140          145          150          155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc 530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80          160          165          170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att 578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84          175          180          185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa 626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190          195          200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act 674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92          205          210          215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag 722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220          225          230          235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa 770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100          240          245          250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc 818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104          255          260          265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg 866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108          270          275          280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc 914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112          285          290          295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc 962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300          305          310          315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa 1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120          320          325          330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act 1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124          335          340          345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt 1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser

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RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:15

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

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128          350          355          360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc 1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132          365          370          375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag 1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380          385          390          395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc 1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140          400          405          410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg 1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144          415          420          425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa 1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148          430          435          440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga 1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152          445          450          455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg 1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460          465          470          475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg 1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160          480          485          490
162 act ccg ggt aaa tgatgactcg acctg 1517
163 Thr Pro Gly Lys
164          495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
W--> 172 <220> FEATURE:
W--> 172 <223> OTHER INFORMATION: see item 6 on Euro Summary Sheet
W--> 172 <400> 2
173 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
174 1          5          10          15
176 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
177          20          25          30
179 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
180          35          40          45
182 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
183          50          55          60
185 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
186 65          70          75          80
188 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
189          85          90          95
191 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
192          100          105          110

```

(same
error in
segs. 4, 6, 8)

RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:15

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

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194 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
195      115      120      125
197 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
198      130      135      140
200 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
201 145      150      155      160
203 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
204      165      170      175
206 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
207      180      185      190
209 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
210      195      200      205
212 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
213      210      215      220
215 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
216 225      230      235      240
218 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
219      245      250      255
221 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
222      260      265      270
224 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225      275      280      285
227 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
228      290      295      300
230 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
231 305      310      315      320
233 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
234      325      330      335
236 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
237      340      345      350
239 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
240      355      360      365
242 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
243      370      375      380
245 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
246 385      390      395      400
248 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
249      405      410      415
251 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
252      420      425      430
254 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
255      435      440      445
257 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
258      450      455      460
260 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
261 465      470      475      480
263 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
264      485      490      495
267 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:15

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

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268 <211> LENGTH: 1485
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence: coding region
274   of SEQ ID NO:1
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)..(1485)
280 <400> SEQUENCE: 3
281 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc 48
282 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
283 1 5 10 15
285 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta 96
286 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
287 20 25 30
289 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag 144
290 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
291 35 40 45
293 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat 192
294 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
295 50 55 60
297 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc 240
298 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
299 65 70 75 80
301 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac 288
302 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
303 85 90 95
305 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag 336
306 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
307 100 105 110
309 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag 384
310 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
311 115 120 125
313 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc 432
314 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
315 130 135 140
317 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat 480
318 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
319 145 150 155 160
321 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct 528
322 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
323 165 170 175
325 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg 576
326 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
327 180 185 190
329 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag 624
330 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
331 195 200 205

```

VERIFICATION SUMMARY

DATE: 12/29/2005

PATENT APPLICATION: US/10/048,116A

TIME: 12:20:16

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12292005\J048116A.raw

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L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
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L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:768